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1: *Virology* 1998 Nov 25;251(2):234-43

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Phylogeographic patterns of feline immunodeficiency virus genetic diversity in the domestic cat.

Carpenter MA, Brown EW, MacDonald DW, O'Brien SJ.

SAIC Frederick, National Cancer Institute-Frederick Cancer Research and Development Center, Frederick, Maryland, 21702-1201, USA.

Feline immunodeficiency virus (FIV) has a worldwide distribution among feral and domesticated cats and in many cases induces immunodeficiency disease analogous to that of human acquired immune deficiency syndrome. FIV is genetically homologous to human immunodeficiency virus (HIV) in both genome organization and gene sequence and, like HIV, exhibits enormous sequence variation throughout the range of host species. We sampled 91 feral cats from six disparate locales and studied the phylogenetic relationships of viral DNA from infected cats using both pol and env genes (520 and 684 bp, respectively). The patterns from the two genes recapitulated previously described major FIV clades and showed concordance between phylogenetic patterns of the pol and env genes. Evidence for recombination between the pol and env genes was not found among a sampling of nine isolates, although evidence for intragenic exchange within the env gene was observed in two isolates. A small local population of cats from a rural farm in the United Kingdom had a remarkably high FIV antibody prevalence (47%), but displayed 8-fold less overall diversity of FIV genomic variation compared with FIV from different parts of the world. We interpret this low variation as a consequence of a recent monophyletic introduction of FIV into the population. Copyright 1998 Academic Press.

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